



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

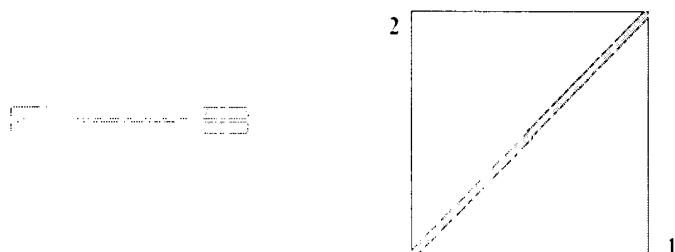
## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

 ALGO: BLOSUM62 ☒ gap open: 11 gap extension: 1

 x\_dropoff: 3% expect: 300 wordsize: 3 Filter: ☐ Align: ☐

Sequence 1 gi: 12312 ATPase, H<sup>+</sup>-transporting, lysosomal, V0 subunit c: ATPase, H<sup>+</sup>-transporting, lysosomal 16kD, V0 subunit c: vacuolar proton pump, 16 kDa subunit: ATPase, H<sup>+</sup>-transporting, lysosomal, 16-KD: vacuolar ATP synthase 16 kDa proteolipid subunit: H<sup>+</sup>-transporting two-sector ATPase, 16 kDa subunit, vacuolar H<sup>+</sup>-ATPase proton channel subunit: ATPase, H<sup>+</sup>-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi: 29950 vacuolar ATPase 16kDa subunit c [Ovis aries] **Length 155 (1..155)**



The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 289 bits (721), Expect = 2e-75  
 Identifier = 151/155 (97%), Positives = 153/155 (98%)

Query: 1 MSESKSGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEQIMKSIIPVV 60

Seq 2: 1 MSE+KSGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEIMKSIIPVV 60

Query: 1 MBEAKSGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEMIMKSIIPVV 60

Seq 2: 1 MBEAKSGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEMIMKSIIPVV 60

Query: 61 MAGIIAIYGLWAVLIANSINDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120

Seq 2: 61 MAGIIAIYGLWAVLIANSINDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120

Query: 61 MAGIIAIYGLWAVLIANSINDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120

Seq 2: 61 MAGIIAIYGLWAVLIANSINDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120

Query: 121 TAQQPRLFGHILTLIFAE'LGLYGLIIVALIILSTK 155

Seq 2: 121 TAQQPRLFGHILTLIFAE'LGLYGLIIVALIILSTK 155

Query: 121 TAQQPRLFGHILTLIFAE'LGLYGLIIVALIILSTK 155

Seq 2: 121 TAQQPRLFGHILTLIFAE'LGLYGLIIVALIILSTK 155

CPUL time: 0.07 user secs. 0.03 sys. secs 0.10 total secs.

Query: 1 H  
 Seq 2: 1 0.140 0.381

Query: 1 H  
 Seq 2: 1 0.041 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 529

Number of Sequences: 0

Number of Extensions: 49

Number of Successful Extensions: 3

Number of sequences better than 300.0: 1  
Number of HSP's better than 300.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 155  
length of database: 428,153,035  
effective HSP length: 115  
effective length of query: 40  
effective length of database: 428,152,920  
effective search space: 17126116800  
effective search space used: 17126116800  
T: 9  
A: 40  
X1: 15 (7.3 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 40 (21.6 bits)  
S2: 55 (25.8 bits)



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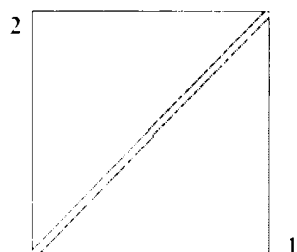
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

gap open: 11 gap extension: 1

x-dropoff: 1 expect: 300.0 wordsize: 3 filter: Align

Sequence 1 gi: 2313 ATPase, H<sup>+</sup>-transporting, lysosomal, V0 subunit c; ATPase, H<sup>+</sup>-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H<sup>+</sup>-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H<sup>+</sup>-transporting two-sector ATPase, 16 kDa subunit; vacuolar H<sup>+</sup>-ATPase proton channel subunit; ATPase, H<sup>+</sup>-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi: 1474 Vacuolar ATP synthase 16 kDa proteolipid subunit *Bovine* **Length 155 (1..155)**



The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 121 bits (718), Expect = 4e-75

Identical = 150/155 (96%), Positives = 153/155 (97%)

```

1  MSESKSGFEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEQIMKS
2  MBE+K+GFEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPE IMKS
3  MBEAKNGFEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEMIMKS
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CPU time: 0.07 user secs. 0.03 sys. secs 0.10 total secs.

Lambda	K	H
0.325	0.141	0.382

## Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 527

Number of Sequences: 3

Number of extensions: 49

Number of successful extensions: 3

Number of sequences better than 300.0: 1

Number of HSP's better than 300.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 155

length of database: 423,153,035

effective HSP length: 115

effective length of query: 40

effective length of database: 426,152,920

effective search space: 17126116800

effective search space used: 17126116800

T: 3

A: 40

K1: 15 ( 7.0 bits)

K2: 129 (49.7 bits)

K3: 129 (49.7 bits)

S1: 40 (21.6 bits)

S2: 55 (25.8 bits)



## Structure

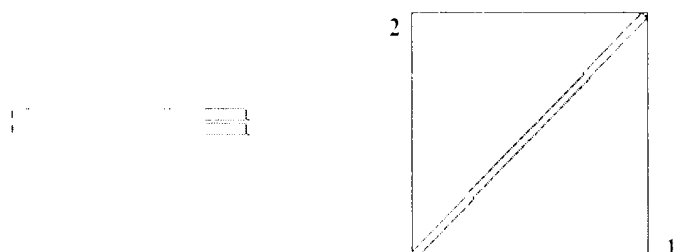
```

- - - - - BLAST find - - - - - gap open: 11 gap extension: 1
- - - - - dropoff: 1 expect: 300.0 wordsize: 3 Filter: Align

```

Length 155 (1 .. 155)

Length 154 (1 .. 154)



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14.14.1.1.1.1 bits (708), Expect = 5e-74
14.14.1.1.1.1 148/153 (96%), Positives = 151/153 (97%)

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T0 = 0.04 user secs.      0.05 sys. secs      0.09 total secs.

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$\frac{1}{2} \times 1.41 = 0.705$

Time (min)	0.410	0.140
1.0	0.000	0.000
2.0	0.000	0.000
3.0	0.000	0.000
4.0	0.000	0.000
5.0	0.000	0.000
6.0	0.000	0.000
7.0	0.000	0.000
8.0	0.000	0.000
9.0	0.000	0.000
10.0	0.000	0.000
11.0	0.000	0.000
12.0	0.000	0.000
13.0	0.000	0.000
14.0	0.000	0.000
15.0	0.000	0.000
16.0	0.000	0.000
17.0	0.000	0.000
18.0	0.000	0.000
19.0	0.000	0.000
20.0	0.000	0.000
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22.0	0.000	0.000
23.0	0.000	0.000
24.0	0.000	0.000
25.0	0.000	0.000
26.0	0.000	0.000
27.0	0.000	0.000
28.0	0.000	0.000
29.0	0.000	0.000
30.0	0.000	0.000
31.0	0.000	0.000
32.0	0.000	0.000
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97.0	0.000	0.000
98.0	0.000	0.000
99.0	0.000	0.000
100.0	0.000	0.000

```

Name: 11_10M62
log Likelihood: Existence: 11, Extension: 1
Number of hits to DB: 525
Number of Sequences: 0
Number of Extensions: 49
Number of successful extensions: 3

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Number of sequences better than 300.0: 1  
Number of HSP's better than 300.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 154  
length of database: 428,153,035  
effective HSP length: 115  
effective length of query: 39  
effective length of database: 428,152,920  
effective search space: 16697963880  
effective search space used: 16697963880  
T: 9  
A: 40  
X1: 15 (7.0 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 40 (21.6 bits)  
S2: 55 (25.3 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

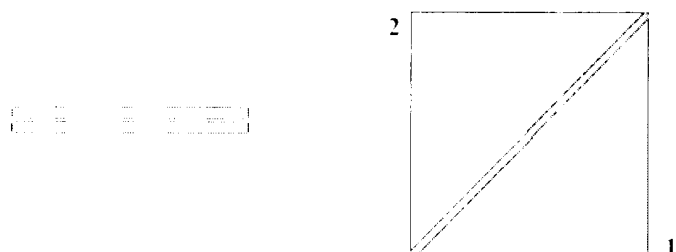
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: BLOSUM62 ☐ gap open: 11 gap extension: 1  
 x-dropoff: 0.05 expect: 300.0 wordsize: 3 Filter: Align

Sequence 1 gi4502313 ATPase, H<sup>+</sup>-transporting, lysosomal, V0 subunit c; ATPase, H<sup>+</sup>-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H<sup>+</sup>-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H<sup>+</sup>-transporting two-sector ATPase, 16 kDa subunit; vacuolar H<sup>+</sup>-ATPase proton channel subunit; ATPase, H<sup>+</sup>-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi109937 H<sup>+</sup>-exporting ATPase (EC 3.6.3.6), vacuolar, 16K chain - mouse *mouse* **Length 155 (1..155)**



The statistics (bit score and expect value) is calculated based on the size of nr database

Score = 166 bits (680), Expect = 1e-70  
 Identities = 147/155 (95%), Positives = 149/155 (96%)

Query: 1 MSESKSGPEYASFFAVMGASAAMVFSALGAAYGTAKSJTGIAAMSVMPFEQIMKSIIPVV 60  
 Subject: 1 MADIENNPEYSSFFGVMGASSAMVFSAMGAAYGTAKSJTGIAAMSVMPFELIMKSIIPVV 60

Query: 61 MAGIHAIVGLVAVLIANSLSLIDISLYHSFLQLGAGLSVGLSGLAAGFAIGIVGDA3VRG 120  
 Subject: 61 MAGIHAIVGLVAVLIANSLSLIDISLYHSFLQLGAGLSVGLSGLAAGFAIGIVGDA3VRG 120

Query: 121 TAAQPPLFVGMILILFAEVLGLYGLIVALILSTK 155  
 Subject: 121 TAAQPPLFVGMILILFAEVLGLYGLIVALILSTK 155

CPUs used: 0.04 user secs. 0.05 sys. secs 0.09 total secs.

Lambda: H H  
 0.001 0.141 0.387

Gap: H H  
 Lambda: H H  
 0.047 0.0410 0.140

Matrix: BLOSUM62

Gap penalties: Existence: 11, Extension: 1

Number of Hits to DB: 532

Number of Sequences: 0

Number of extensions: 51

Number of successful extensions: 3

Number of sequences better than 300.0: 1  
Number of HSP's better than 300.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 155  
length of database: 428,153,035  
effective HSP length: 115  
effective length of query: 40  
effective length of database: 428,152,920  
effective search space: 17126116800  
effective search space used: 17126116800  
T: 9  
A: 40  
X1: 15 (7.3 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 40 (21.6 bits)  
S2: 55 (25.3 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

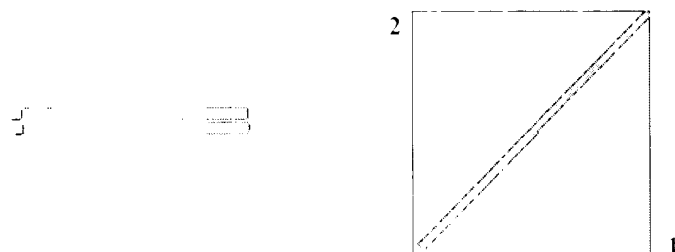
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

☐ BLAST 2 ☒ gap open: 11 gap extension: 1

☐ dropoff: 2 expect: 300 wordsize: 2 Filter: Align

Sequence 1 gi: 12512 ATPase, H<sup>+</sup>-transporting, lysosomal, V0 subunit c; ATPase, H<sup>+</sup>-transporting, lysosomal 16kD, V0 subunit c, vacuolar proton pump, 16 kDa subunit; ATPase, H<sup>+</sup>-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H<sup>+</sup>-transporting two-sector ATPase, 16 kDa subunit, vacuolar H<sup>+</sup>-ATPase proton channel subunit; ATPase, H<sup>+</sup>-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 gi: 141 15 kDa protein [Torpedo marmorata] **Length 154 (1..154)**



The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 148 bits (671), Expect = 1e-69  
 Identities = 140/148 (94%), Positives = 145/148 (97%)



Query: 1 MHYASFFAVMGASAAMVFSALGAAYGTAKSSTGIAAMSVMRPEQIMKSIIPVVMAGIITAI 67  
 Ref: 1 MHY++FF V+GASAAMVFSALGAAYGTAKSSTGIAAMSVMRPE IMKSIIPVVMAGIITAI  
 Query: 2 MHYSAFFGVIGASAAMVFSALGAAYGTAKSSTGIAAMSVMRPELIMKSIIPVVMAGIITAI 66

Query: 127 YNLWVAVLIANSNLDELFLYKSFLLQGLSVGLSGLAAGFAIGIVGDAGVRGTAQQPRL 127  
 Ref: 127 YNLWVAVLIANSL +LFL+KSFLLQGLSVGLSGLAAGFAIGIVGDAGVRGTAQQPRL  
 Query: 126 YNLWVAVLIANSLTDELFLKSFLLQGLSVGLSGLAAGFAIGIVGDAGVRGTAQQPRL 126

Query: 154 FTGMILILIFAENVLGLYGLIIVALILSTH 155  
 Ref: 154 FTGMILILIFAENVLGLYGLIIVALILSTH  
 Query: 153 FTGMILILIFAENVLGLYGLIIVALILSTH 154

Performance: 0.04 user secs. 0.05 sys. secs 0.09 total secs.

Length: 155 H  
 0.115 0.142 0.387

Length: 154 H  
 0.115 0.0410 0.140

Database: BLAST/BLAST

Number of hits: Existence: 11, Extension: 1  
 Number of hits to DB: 516  
 Number of sequences: 0  
 Number of extensions: 48  
 Number of successful extensions: 3

Number of sequences better than 300.0: 1  
Number of HSP's better than 300.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 154  
length of database: 428,153,035  
effective HSP length: 115  
effective length of query: 39  
effective length of database: 428,152,920  
effective search space: 16697963880  
effective search space used: 16697963880  
T: 9  
A: 40  
X1: 15 (7.0 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 40 (21.6 bits)  
S2: 55 (25.8 bits)

**PubMed**

BLAST SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

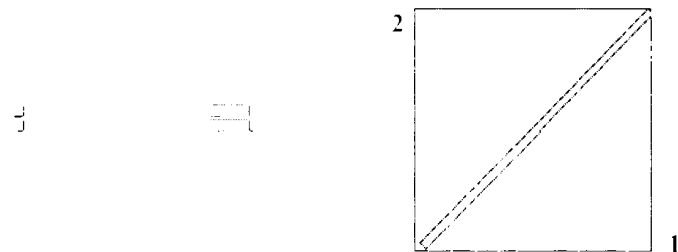
```

11.1.1.1 BLASTn 2.2.26 gap open: 11 gap extension: 1
x_dropoff: 0.2 expect: 300.0 wordsize: 3 Filter Align

```

<b>Sequence ID</b>	Q113	<b>Length</b>	155 (1..155)
<p>ATPase, H<sup>+</sup>-transporting, lysosomal, V0 subunit c; ATPase, H<sup>+</sup>-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H<sup>+</sup>-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H(+)-transporting two-sector ATPase, 16 kDa subunit; vacuolar H<sup>+</sup>-ATPase proton channel subunit; ATPase, H<sup>+</sup>-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens]</p>			

**Sequence** 2: [cp\\_00786.vacuoar ATP synthase 16 kDa proteolipid subunit \[Danio rerio\]](#) **Length** 154 (1 .. 154)

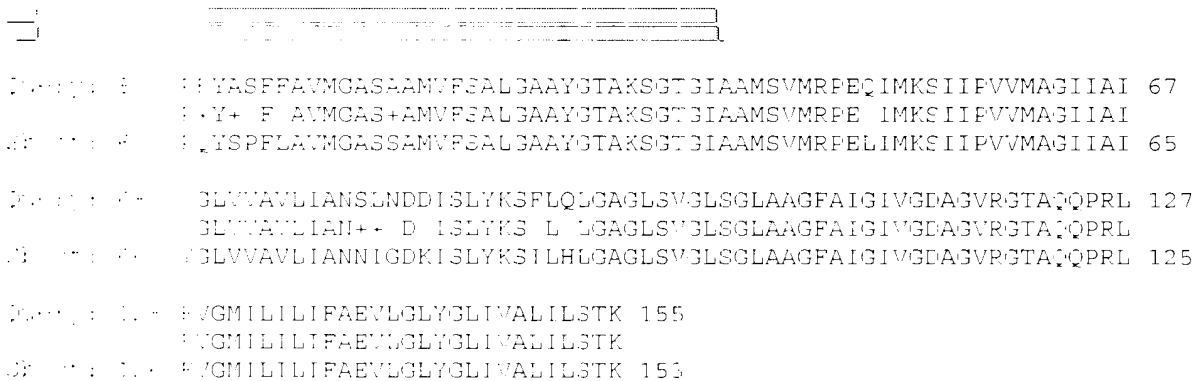


The statistics (bitscore and expect value) is calculated based on the size of nr database

```

# of bits (650), Expect = 3e-67
# of bits (136/148 (91%), Positives = 141/143 (94%)

```



```

0.04 user secs.      0.05 sys. secs      0.09 total secs.

```

DATE: 11/11/1971	TIME: 11:00	BY: H
1. 1. 1	0.142	0.389

1.  $\frac{1}{2}$

```
Material: BILUM62  
Gd Data Files: Existence: 11, Extension: 1  
Number of hits to DB: 506  
Number of sequences: 0  
Number of extensions: 54
```

Number of successful extensions: 3  
Number of sequences better than 300.0: 1  
Number of HSP's better than 300.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 154  
length of database: 428,153,035  
effective HSP length: 115  
effective length of query: 39  
effective length of database: 428,152,920  
effective search space: 16697963880  
effective search space used: 16697963880  
T: 9  
A: 40  
X1: 15 (7.0 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 40 (21.5 bits)  
S2: 55 (25.8 bits)



## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

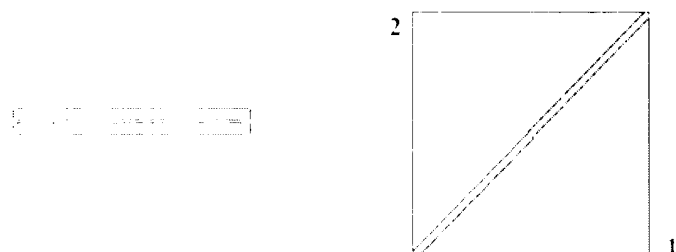
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: BLOSUM62 ☐ gap open: 11 gap extension: 1

X-dropoff: 50 expect: 300.0 wordsize: 3 Filter: Align

Sequence 1 (gi: 10331) ATPase, H<sup>+</sup>-transporting, lysosomal, V0 subunit c; ATPase, H<sup>+</sup>-transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H<sup>+</sup>-transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H<sup>+</sup>-transporting two-sector ATPase, 16 kDa subunit, vacuolar H<sup>+</sup>-ATPase proton channel subunit; ATPase, H<sup>+</sup>-transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens] **Length 155 (1..155)**

Sequence 2 (gi: 954) H<sup>+</sup>-exporting ATPase (EC 3.6.3.6), vacuolar, 16K chain - bovine **Length 155 (1..155)**



The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 113 bits (646), Expect = 9e-67

Identities = 138/155 (89%), Positives = 143/155 (92%)

```

Query: 1      MSSEKSGPEYASFFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEQIMKSIIPVV 60
             MSSE+K+GPEYASFFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPE IMKSIIPVV
Sbjct: 1      MSSEAKNGPEYASFFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEMIMKSIIPVV 60

Query: 61     MAGHIAIYGLVVAVLIA NSLNDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRG 120
             MAGHIAIYGLVVAVLIA NSLNDDISLY+SFLLQLGAGLSVGLSGLAA ++G G
Sbjct: 61     MAGHIAIYGLVVAVLIA NSLDGISLYPSFLQLGAGLSVGLSGLAARSPSALLGTQGRAC 120

Query: 121    TAQQPPLFVGMILILIFA EVLGLYGLIVALILSTK 155
             TAQQPPLFVGMILILIFA EVLGLYGLIVALILSTK
Sbjct: 121    TAQQPPLFVGMILILIFA EVLGLYGLIVALILSTK 155

```

CPU time: 0.08 user secs. 0.00 sys. secs 0.08 total secs.

Length: 155 H  
 0.24 0.138 0.375

Gaps: 0  
 Length: 155 H  
 0.07 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of hits to DB: 490

Number of sequences: 9

Number of extensions: 42

Number of successful extensions: 3

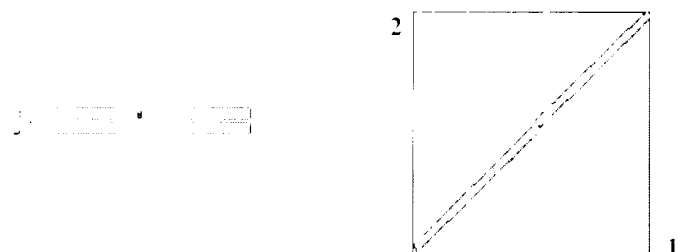
Number of sequences better than 300.0: 1  
Number of HSP's better than 300.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non prelim): 1  
length of query: 155  
length of database: 428,153,035  
effective HSP length: 115  
effective length of query: 40  
effective length of database: 428,152,920  
effective search space: 17126116800  
effective search space used: 17126116800  
T: 9  
A: 40  
X1: 15 (7.0 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 40 (21.6 bits)  
S2: 55 (25.8 bits)

## Blast 2 Sequences results

## Structure

## x\_dropoff: 7 expect: 300, wordsize: 3 letter Align

<b>Sequence 1</b> (gi: 12312)	ATPase, H <sup>+</sup> -transporting, lysosomal, V0 subunit c; ATPase, H <sup>+</sup> -transporting, lysosomal 16kD, V0 subunit c; vacuolar proton pump, 16 kDa subunit; ATPase, H <sup>+</sup> -transporting, lysosomal, 16-KD; vacuolar ATP synthase 16 kDa proteolipid subunit; H <sup>(+)</sup> -transporting two-sector ATPase, 16 kDa subunit; vacuolar H <sup>+</sup> -ATPase proton channel subunit; ATPase, H <sup>+</sup> -transporting, lysosomal (vacuolar proton pump) 16kD [Homo sapiens]	<b>Length</b> 155 (1..155)
<b>Sequence 2</b> (gi: 112)	H <sup>(+)</sup> -ATPase [Drosophila melanogaster]	<b>Length</b> 159 (1..159)



```

Length = 135 bits (59%), Expect = 1e-60
Identical = 125/154 (81%), Positives = 135/154 (89%), Gaps = 2/154 (1%)

```



Query: 4	MSHGPEYASFFAVMGASAAMVFSALGAAYGTAKSGTGIAAMSVMRPEQIMKSIIPVVMAG	63
	3 P Y FF VMGA++A++FSALGAAYGTAKSGTGIAAMSVMRPE IMKSIIPVVMAG	
Ref: 1	MDNPLITGPPFGVMGAASATFSALGAAYGTAKSGTGIAAMSVMRPELIMKSIIPVVMAG	65
Query: 64	MAITGLNVAVLIAHSLND--DLSLYKSFQLGAGLSVGLSGLAAGFAIGIVGDAGVRGT	121
	MAITGLNVAVLIA +L - SLY+ F+ LGAGL+VG SGLAAGFAIGIVGDAGVRGT	
Ref: 1	MAITGLNVAVLIAGALEEPSKYSLYPGFIHLGAGLAVGFSGLAAGFAIGIVGDAGVRGT	125
Query: 111	AIQPREFVGMILILIFAEVLGLYGLIVAILSTK	155
	AIQPREFVGMILILIFAEVLGLYGLIVA+ L TK	
Ref: 1	AIQPREFVGMILILIFAEVLGLYGLIVAIYLYTK	159

```

%*** time:      0.06 user secs.      0.03 sys. secs      0.09 total secs.

```

Gamma	$\gamma$	H
0.12:	0.140	0.375

Quoted		
Lambda	$\epsilon$	H
0.26	0.0410	0.140

Matrix: ILI\_SUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of hits to DB: 556  
Number of sequences: 0  
Number of extensions: 60  
Number of successful extensions: 4

Number of sequences better than 300.0: 1  
Number of HSP's better than 300.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 155  
length of database: 428,153,035  
effective HSP length: 115  
effective length of query: 40  
effective length of database: 428,152,920  
effective search space: 17126116800  
effective search space used: 17126116800  
T: 9  
A: 40  
X1: 15 (7.0 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 41 (22.0 bits)  
S2: 55 (25.8 bits)





PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search Nucleotide ☐ for  Go Clear  
Limits Preview/Index History Clipboard Details  
Display default ☐ Show: 20 ☐ Send to File ☐ Get Subsequence

1: AC015913. Homo sapiens chro...[gi:16506451]

Links

LOCUS AC015913 184595 bp DNA linear HTG 05-AUG-2002  
DEFINITION Homo sapiens chromosome 17 clone RP11-81A22 map 17, WORKING DRAFT  
SEQUENCE, 32 unordered pieces.  
ACCESSION AC015913  
VERSION AC015913.3 GI:16506451  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 184595)  
AUTHORS Birren,B., Nusbaum,C. and Lander,E.  
TITLE Homo sapiens chromosome 17, clone RP11-81A22  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 184595)  
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
Baldwin,J., Barna,H., Beckerly,R., Boguslavskiy,L., Boukhgalter,B.,  
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,  
Coode,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
Ferreira,P., FitzHugh,W., Forrest,C., Funke,P., Gage,D.,  
Galagan,J., Gardina,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Johnson,P., Jones,C., Kann,L., Karatas,A., Klein,J.,  
Lehoczky,J., Liem,C., Locke,K., Macdonald,P., Marquis,N.,  
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,  
Morrow,C., Naylor,T., Norman,C.H., O'Connor,T., O'Donnell,P.,  
Peterson,K., Poltara,V., Piley,E., Roy,A., Santos,R., Severy,P.,  
Stange Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
Tefaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
TITLE Direct Submission  
JOURNAL Submitted (17 NOV 1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
REFERENCE 3 (bases 1 to 184595)  
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barna,H., Bastien,T., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,  
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,  
Coode,A., Coode,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,  
Gardina,S., Gard,S., Graham,L., Grand Pierre,N., Hagos,B.,  
Horton,L., Humme,W., Iliev,I., Johnson,P., Jones,C., Kamat,A.,  
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,  
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,  
Murphy,T., Naylor,T., Nguyen,C., Nicol,F., Norbu,C., Norman,C.H.,  
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,  
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Roy,A., Schauer,S., Schupbach,R., Seaman,S., Severy,P.,  
Smith,C., Spencer,E., Stange Thomann,N., Stojanovic,N., Talamas,J.,  
Tefaye,S., Theodores,J., Topham,F., Travers,H., Vassiliev,H.,  
Vieira,E., Vo,A., Weller,B., Wu,X., Wyman,D., Young,G., Zaimoun,J.,  
Zemick,L., Zimmer,A. and Zody,M.  
TITLE Direct Submission  
JOURNAL Submitted (06 AUG 2002) Whitehead Institute/MIT Center for Genome

## COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Oct 27, 2001 this sequence version replaced gi:16356913.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www.seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

## ----- Project Information

Center project name: L938  
Center clone name: 31\_A\_21

## ----- Summary Statistics

Sequencing vector: M13; M77815; 40% of reads  
Sequencing vector: Plasmid; n/a; 60% of reads  
Chemistry: Dye-primer-amersham; 2% of reads  
Chemistry: Dye-terminator Big Dye; 98% of reads  
Assembly program: Ehhap; version 0.960731  
Consensus quality: 168221 bases at least Q40  
Consensus quality: 175650 bases at least Q30  
Consensus quality: 178768 bases at least Q20  
Insert size: 203000; agarose-ff  
Insert size: 181495; sum-of-contigs  
Quality coverage: 7.6 in Q20 bases.

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 31 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\*       1       11663: contig of 10663 bp in length  
\*       10664 10763: gap of       100 bp  
\*       10764       11382: contig of 619 bp in length  
\*       11393 11492: gap of       100 bp  
\*       11493       12333: contig of 840 bp in length  
\*       12334 12433: gap of       100 bp  
\*       12434       13332: contig of 899 bp in length  
\*       13333 13432: gap of       100 bp  
\*       13433       14716: contig of 1384 bp in length  
\*       14717 14816: gap of       100 bp  
\*       14817       16101: contig of 1285 bp in length  
\*       16102 16201: gap of       100 bp  
\*       16202       17797: contig of 1596 bp in length  
\*       17798 17897: gap of       100 bp  
\*       17898       18949: contig of 1151 bp in length  
\*       18950 19049: gap of       100 bp  
\*       19050       20494: contig of 1444 bp in length  
\*       20495 20594: gap of       100 bp  
\*       20595       21778: contig of 1183 bp in length  
\*       21779 21878: gap of       100 bp  
\*       21879       23459: contig of 1580 bp in length  
\*       23460 23559: gap of       100 bp  
\*       23560       25831: contig of 2272 bp in length  
\*       25832 25931: gap of       100 bp  
\*       25932       27763: contig of 1832 bp in length  
\*       27764 27863: gap of       100 bp  
\*       27864       29986: contig of 2123 bp in length  
\*       29987 30086: gap of       100 bp  
\*       30087       32675: contig of 2589 bp in length  
\*       32676 32775: gap of       100 bp  
\*       32776       36266: contig of 3491 bp in length  
\*       36267 36366: gap of       100 bp



# Nucleotide

PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
Search	for	for	for	for	for	for	for	for
Display	Show: 20	Send to	File	Get Subsequence				

1: AC015913 Homo sapiens chro...[gi:16506451]

Links

LOCUS AC015913 184595 bp DNA linear HTG 05-AUG-2002  
 DEFINITION Homo sapiens chromosome 17 clone RP11-81A22 map 17, WORKING DRAFT  
 SEQUENCE, 30 unordered clones.

AC015913

AC015913.3 GI:16506451

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_18AFT; HTGS\_FULLTOP.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Phylum: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REPERENNIAL bases 1 to 184595

AUTHOR Pirren, E., Nisbaum, C. and Lander, E.

TITLE Homo sapiens chromosome 17, clone RP11-81A22

JOURNAL Unpublished

REPERENNIAL bases 1 to 184595

AUTHOR Pirren, E., Linton, L., Nisbaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baldwin, J., Barna, N., Barkerly, R., Boguslavskiy, L., Bolikhgalter, B.,  
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
 Cooke, P., DeArnelland, K., Dewar, K., Domino, M., Dorcelan, L., Doyle, M.,  
 Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,  
 Galagan, J., Gardina, S., Grant, G., Haggis, B., Heaford, A., Horton, L.,  
 Howland, J.C., Johnson, R., Jones, C., Kahr, L., Karatas, A., Klein, J.,  
 Lehtozky, J., Liew, C., Locke, K., MacDonald, P., Marquis, N.,  
 McEwan, P., McDuck, A., McVernan, K., McLaughlin, J., Melarim, J.,  
 Morris, J., Naylor, C., Norman, C.H., O'Connor, T., O'Donnell, P.,  
 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
 Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, C., Wu, X.,  
 Wyman, D., Ye, W.C., Zimmer, A. and Zody, M.

TITLE Direct Submission

JOURNAL Submitted (17 NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 300 Charles Street, Cambridge, MA 02141, USA

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AUTHOR Pirren, E., Nisbaum, C., Lander, E., Allen, N., Anderson, S.,  
 Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Bolikhgalter, B.,  
 Chamarata, J., Chang, C., Chazaro, B., Choepel, Y., Collymore, A.,  
 Cooke, A., Cooke, P., DeArnelland, K., Dewar, K., Diaz, J.S., Dodge, S.,  
 Fano, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,  
 Gardina, S., Gerd, S., Graham, L., Grand Pierre, N., Haggis, B.,  
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,  
 Karatas, A., Kells, C., Lenders, T., Levine, R., Lindblad-Toh, K.,  
 Liu, G., MacLean, C., MacDonald, P., Major, J., Matthews, C.,  
 McCarthy, M., Melarim, J., Meneus, L., Kinova, T., Klenga, V.,  
 Murphy, T., Naylor, J., Naylor, C., Nicol, R., Norbu, C., Norman, C.H.,  
 O'Connor, T., O'Donnell, P., O'Neil, E., Oliver, C., Peterson, K.,  
 Phunghang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
 Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,  
 Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Talamas, J.,  
 Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
 Tiel, P., Vo, A., Wilson, J., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
 Zemzek, L., Zimmer, A. and Zody, M.

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## COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Oct 27, 2001 this sequence version replaced gi:16506451.  
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)  
<http://www.genome.wi.mit.edu/RepeatMasker.html>

Center: Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBA

Web site: <http://www.seq.wi.mit.edu>

Contact: [sequence\\_submissions\\_genome.wi.mit.edu](mailto:sequence_submissions_genome.wi.mit.edu)

Project Information

Center project name: L834

Center clone name: 31\_A\_12

Summary Statistics

Sequencing vector: M13; M77311; 41% of reads

Sequencing vector: Plasmid; n/a; 60% of reads

Chemistry: Dye-primer-amersham; 2% of reads

Chemistry: Dye-terminator Big Dye; 98% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 168221 bases at least Q40

Consensus quality: 175652 bases at least Q30

Consensus quality: 178769 bases at least Q20

Insert size: 213101; agarose-gel

Insert size: 181499; sum-of-contigs

Quality coverage: 7.6 in 220 bases.

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 31 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 13663: contig of 13663 bp in length  
 \* 11364 11761: gap of 100 bp  
 \* 11764 11891: contig of 119 bp in length  
 \* 11191 11491: gap of 100 bp  
 \* 11491 11531: contig of 41 bp in length  
 \* 11534 12433: gap of 100 bp  
 \* 12434 13331: contig of 897 bp in length  
 \* 13331 14431: gap of 100 bp  
 \* 14431 14714: contig of 284 bp in length  
 \* 14717 14814: gap of 100 bp  
 \* 14817 16101: contig of 1284 bp in length  
 \* 16101 16201: gap of 100 bp  
 \* 16201 17797: contig of 1596 bp in length  
 \* 17797 17897: gap of 100 bp  
 \* 17897 18943: contig of 1056 bp in length  
 \* 18943 19043: gap of 100 bp  
 \* 19043 20494: contig of 1451 bp in length  
 \* 20495 20594: gap of 100 bp  
 \* 20595 21775: contig of 1181 bp in length  
 \* 21775 21875: gap of 100 bp  
 \* 21875 23433: contig of 1558 bp in length  
 \* 23433 23533: gap of 100 bp  
 \* 23533 23831: contig of 298 bp in length  
 \* 23831 23931: gap of 100 bp  
 \* 23931 27763: contig of 3832 bp in length  
 \* 27764 27863: gap of 100 bp  
 \* 27864 29986: contig of 2123 bp in length  
 \* 29987 30086: gap of 100 bp  
 \* 30087 32675: contig of 2588 bp in length  
 \* 32676 32775: gap of 100 bp  
 \* 32776 36266: contig of 3491 bp in length  
 \* 36267 36366: gap of 100 bp